

# FIGURE 1

1 GAACCAGCCT GCACGCGCTG GCTCCGGGTG ACAGCCGCGC GCCTCGGCCA  
 51 GGATCTGAGT GATGAGACGT GTCCCCACTG AGGTGCCCCA CAGCAGCAGG  
 101 TGTTGAGCAT GGGCTGAGAA GCTGGACCGG CACCAAAGGG CTGGCAGAAA  
 151 TGGGCGCCTG GCTGATTCTT AGGCAGTTGG CGGCAGCAAG GAGGAGAGGC  
 201 CGCAGCTTCT GGAGCAGAGC CGAGACGAAG CAGTTCTGGA GTGCCTGAAC  
 251 GGCCCCCTGA GCCCTACCCG CCTGGCCAC TATGGTCCAG AGGCTGTGGG  
 301 TGAGCCGCTT GCTGCGGCAC CGGAAAGCCC AGCTCTTGCT GGTCAACCTG  
 351 CTAACCTTTG GCCTGGAGGT GTGTTTGGCC GCAGGCATCA CCTATGTGCC  
 401 GCCTCTGCTG CTGGAAGTGG GGGTAGAGGA GAAGTTCATG ACCATGGTGC  
 451 TGGGCATTGG TCCAGTGCTG GGCCTGGTCT GTGTCCCGCT CCTAGGCTCA  
 501 GCCAGTGACC ACTGGCGTGG ACGCTATGGC CGCCGCCGGC CCTTCATCTG  
 551 GGCAGTGTCC TTGGGCATCC TGCTGAGCCT CTTTCTCATC CCAAGGGCCG  
 601 GCTGGCTAGC AGGGCTGCTG TGCCCGGATC CCAGGCCCCCT GGAGCTGGCA  
 651 CTGCTCATCC TGGGCGTGGG GCTGCTGGAC TTCTGTGGCC AGGTGTGCTT  
 701 CACTCCACTG GAGGCCCTGC TCTCTGACCT CTTCCGGGAC CCGGACCACT  
 751 GTCGCCAGGC CTACTCTGTC TATGCCTTCA TGATCAGTCT TGGGGGCTGC  
 801 CTGGGCTACC TCCTGCCTGC CATTGACTGG GACACCAGTG CCCTGGCCCC  
 851 CTACCTGGGC ACCCAGGAGG AGTGCCTCTT TGGCCTGCTC ACCCTCATCT  
 901 TCCTCACCTG CGTAGCAGCC ACACTGCTGG TGGCTGAGGA GGCAGCGCTG  
 951 GGCCCCACCG AGCCAGCAGA AGGGCTGTCT GCCCCCTCCT TGTCGCCCCA  
 1001 CTGCTGTCCA TGCCGGGCCC GCTTGGCTTT CCGGAACCTG GGCGCCCTGC  
 1051 TTCCCCGGCT GCACCAGCTG TGCTGCCGCA TGCCCCGCAC CCTGCGCCGG  
 1101 CTCTTCGTGG CTGAGCTGTG CAGCTGGATG GCACTCATGA CCTTCACGCT  
 1151 GTTTTACACG GATTTCGTGG GCGAGGGGCT GTACCAGGGC GTGCCCAGAG  
 1201 CTGAGCCGGG CACCGAGGCC CGGAGACACT ATGATGAAGG CGTTCGGATG  
 1251 GGCAGCCTGG GGCTGTTCTT GCAGTGCGCC ATCTCCCTGG TCTTCTCTCT  
 1301 GGTCATGGAC CGGCTGGTGC AGCGATTCGG CACTCGAGCA GTCTATTGGA  
 1351 CCAGTGTGGC AGCTTTCCCT GTGGCTGCCG GTGCCACATG CCTGTCCCAC  
 1401 AGTGTGGCCG TGGTGACAGC TTCAGCCGCC CTCACCGGGT TCACCTTCTC

# FIGURE 1 – continued

1451 AGCCCTGCAG ATCCTGCCCT ACACACTGGC CTCCTCTAC CACCGGGAGA  
 1501 AGCAGGTGTT CCTGCCCCAA TACCGAGGGG ACACTGGAGG TGCTAGCAGT  
 1551 GAGGACAGCC TGATGACCAG CTTCTGCCA GGCCCTAAGC CTGGAGCTCC  
 1601 CTTCCCTAAT GGACACGTGG GTGCTGGAGG CAGTGGCCTG CTCCCACCTC  
 1651 CACCCGCGCT CTGCGGGGCC TCTGCCTGTG ATGTCTCCGT ACGTGTGGTG  
 1701 GTGGGTGAGC CCACCGAGGC CAGGGTGGTT CCGGGCCGGG GCATCTGCCT  
 1751 GGACCTCGCC ATCCTGGATA GTGCCTTCCT GCTGTCCCAG GTGGCCCCAT  
 1801 CCCTGTTTAT GGGCTCCATT GTCCAGCTCA GCCAGTCTGT CACTGCCTAT  
 1851 ATGGTGTCTG CCGCAGGCCT GGGTCTGGTC GCCATTTACT TTGCTACACA  
 1901 GGTAGTATTT GACAAGAGCG ACTTGCCAA ATACTCAGCG TAGAAAACTT  
 1951 CCAGCACATT GGGGTGGAGG GCCTGCCTCA CTGGGTCCCA GCTCCCCGCT  
 2001 CCTGTTAGCC CCATGGGGCT GCCGGGCTGG CCGCCAGTTT CTGTTGCTGC  
 2051 CAAAGTAATG TGGCTCTCTG CTGCCACCCT GTGCTGCTGA GGTGCGTAGC  
 2101 TGCACAGCTG GGGGCTGGGG CGTCCCTCTC CTCTCTCCCC AGTCTCTAGG  
 2151 GCTGCCTGAC TGGAGGCCTT CCAAGGGGGT TTCAGTCTGG ACTTATACAG  
 2201 GGAGGCCAGA AGGGCTCCAT GCACTGGAAT GCGGGGACTC TGCAGGTGGA  
 2251 TTACCCAGGC TCAGGGTTAA CAGCTAGCCT CCTAGTTGAG ACACACCTAG  
 2301 AGAAGGGTTT TTGGGAGCTG AATAAACTCA GTCACCTGGT TTCCCATCTC  
 2351 TAAGCCCCTT AACCTGCAGC TTCGTTTAAT GTAGCTCTTG CATGGGAGTT  
 2401 TCTAGGATGA AACACTCCTC CATGGGATTT GAACATATGA AAGTTATTTG  
 2451 TAGGGGAAGA GTCCTGAGGG GCAACACACA AGAACCAGGT CCCCTCAGCC  
 2501 CACAGCACTG TCTTTTTGCT GATCCACCCC CTTCTTACCT TTTATCAGGA  
 2551 TGTGGCCTGT TGGTCCTTCT GTTGCCATCA CAGAGACACA GGCATTTAAA  
 2601 TATTTAACTT ATTTATTTAA CAAAGTAGAA GGAATCCAT TGCTAGCTTT  
 2651 TCTGTGTTGG TGTCTAATAT TTGGGTAGGG TGGGGGATCC CCAACAATCA  
 2701 GGTCCCCTGA GATAGCTGGT CATTGGGCTG ATCATTGCCA GAATCTTCTT  
 2751 CTCCTGGGGT CTGGCCCCCC AAAATGCCTA ACCCAGGACC TTGGAAATTC  
 2801 TACTCATCCC AAATGATAAT TCCAAATGCT GTTACCCAAG GTTAGGGTGT

## FIGURE 1 - continued

2851 TGAAGGAAGG TAGAGGGTGG GGCTTCAGGT CTCAACGGCT TCCCTAACCA  
2901 CCCCTCTTCT CTTGGCCCAG CCTGGTTCCC CCCACTTCCA CTCCCCTCTA  
2951 CTCTCTCTAG GACTGGGCTG ATGAAGGCAC TGCCCCAAAAT TTCCCCTACC  
3001 CCCAACTTTC CCCTACCCCC AACTTTCCCC ACCAGCTCCA CAACCCTGTT  
3051 TGGAGCTACT GCAGGACCAG AAGCACAAAG TGCGGTTTCC CAAGCCTTTG  
3101 TCCATCTCAG CCCCCAGAGT ATATCTGTGC TTGGGGAATC TCACACAGAA  
3151 ACTCAGGAGC ACCCCCTGCC TGAGCTAAGG GAGGTCTTAT CTCTCAGGGG  
3201 GGGGTTTAAAG TGCCGTTTGC AATAATGTCG TCTTATTTAT TTAGCGGGGT  
3251 GAATATTTTA TACTGTAAGT GAGCAATCAG AGTATAATGT TTATGGTGAC  
3301 AAAATTAAAG GCTTTCCTTAT

[illegible]

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1 MVQRLWVSRL LRHRKAQLLLNLLTFGLV CLAAGITYVP PLLLEVGVVEE
51 KFMTMVLGIG PVLGLVCVPL LGSASDHWRG RYGRRRPFIW ALSLGILLSL
101 FLIPRAGWLA GLLCPDPRPL ELALLILGVG LLDFCGQVCF TPLEALLSDL
151 FRDPDHCRQA YSVYAFMISL GGCLGYLLPA IDWDTSALAP YLGTQEECLF
201 GLLTLIFLTC VAATLLVAEE AALGPTEPAE GLSAPSLSPH CCPCRARLAF
251 RNLGALLPRL HQLCCRMPT LRRLFVAELC SWMALMTFTL FYTDFVGEGL
301 YQGVPRAEFG TEARRHYDEG VRMGSLGLFL QCAISLVFSL VMDRLVQRFG
351 TRAVYLASVA AFPVAAGATC LSHSVAVVTA SAALTGFTEF ALQILPYTLA
401 SLYHREKQVF LPKYRGDTGG ASSEDSLMTS FLPGPKPGAP FPNGHVGAGG
451 SGLLPPPPAL CGASACDVSF RVVVGEPTFA RVVPGRGICL DLAILDSAFL
501 LSQVAPSLFM GSIVQLSQSV TAYMVSAAGL GLVAIVFATQ VVFDKSDLAK
551 YSA

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FIGURE 3

DcSUT2 1 MENGTKELNKPQPPSSAAMQLQTPVQKIPTATWKLVLVAAIAAGVQFGWA 50  
PROST03 1 .....MVQRLWVSRLLRHRKAQLLLVNLLTFGLEVCLA 33  
51 LQLSLLTPYVQLLGIPHKWAAIWLCPISGMLVQPIVGYYSDHCQSSFG 100  
34 AGITYVPPLLLLEVGVEEKFMTMVLGIGPVLGLVCVPLLGSASDHWRGRYG 83  
101 RRRPFIASGAGCVAISVILIGFAADISYKAGDDMSKTLKPRAVTVFVIGF 150  
84 RRRPFIWALSGLLSLFLIPRAGWLAGLLCPDP....RPLELALLILGV 129  
151 WILDVANMLQGPCRALLADLCSGDTRRMRSANAFYSFFMAVGNILGYAA 200  
130 GLLDFCGQVCFTPLEALLSDLFR.DPDHCRQAYSVYAFMISLGGCLGYLL 178  
201 GSYN.NLYKLFPFSKTHACDLYCANLKSCFIISIALLIITVVALSVVRE 249  
179 PAIDWDTSALAPYLGTQEELFGLLTLIFLTCVAATLLVAEEAALGPTEP 228  
250 NSGPPDDADAAEPPSSGKIPV..FGELLGALKDL....PRPMLLLLIIVT 293  
229 AEGLSAPSLSPHCCPCRARLAFRNLGALLPRLHQLCCRMPTLRRLFVAE 278  
294 CLNWIAWFPFILFDTDWMGREIYGGT.....AGQGKLYDQGVVAGALGL 337  
279 LCSWMALMTFTLFYTDVFGELYQGVPRAEPTARRHYDEGVRMGSLGL 328  
338 LLNSVVLGLTSIAVEYLVRGVGVVKILWGFVNFILAIGLMTVVVSKVAQ 387  
329 FLQCAISLVFSLVMDRLVQRFGTRAV.....YLASVAAFPVAA 366  
388 HQREHSANGQLLPPSAGVKAGALSLSILGIPLSITYSIPFALASIYSSG 437  
367 GATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRG 416  
438 SGAGQGLSLGVLNLAIVVPQMIVSVLAGPFDLSLFGGGLNLPFVVGAISAA 487  
417 DTGGASSEDLSMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASAC 466  
488 ISGVLAIVLLPKPSKDAASKLSLSGTYH..... 515  
467 DVSVRVVVGEPTARVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIVQL 516

1000  
900  
800  
700  
600  
500  
400  
300  
200  
100  
0

FIGURE 4

GAACCAGCCTGCACGCGCTGGCTCCGGGTGACAGCCGCGCCTCGGCCAGGATCTGAGT  
1 -----+-----+-----+-----+-----+-----+ 60  
CTTGGTCGGACGTGCGCGACCGAGGCCACTGTGCGCGCGGAGCCGGTCTAGACTCA

GATGAGACGTGTCCCCACTGAGGTGCCCCACAGCAGCAGGTGTTGAGCATGGGCTGAGAA  
61 -----+-----+-----+-----+-----+-----+ 120  
CTACTCTGCACAGGGGTGACTCCACGGGGTGTCTGCTCCACAACCTCGTACCCGACTCTT

GCTGGACCGGCACCAAAGGGCTGGCAGAAATGGGCGCCTGGCTGATTCTAGGCAGTTGG  
121 -----+-----+-----+-----+-----+-----+ 180  
CGACCTGGCCGTGGTTTCCCGACCGTCTTACCCGCGGACCGACTAAGGATCCGTCAACC

CGGCAGCAAGGAGGAGAGGCCGAGCTTCTGGAGCAGAGCCGAGACGAAGCAGTTCTGGA  
181 -----+-----+-----+-----+-----+-----+ 240  
GCCGTCGTTCTCTCTCCGGCGTCGAAGACCTCGTCTCGGCTCTGCTTCGTCAAGACCT

GTGCCTGAACGGCCCCCTGAGCCCTACCCGCTGGCCCACTATGGTCCAGAGGCTGTGGG  
241 -----+-----+-----+-----+-----+-----+ 300  
CACGGACTTGCCGGGGGACTCGGGATGGGCGGACCGGGTGATACCAGGTCTCCGACACC

c M V Q R L W V -

TGAGCCGCTGCTGCGGCACCGGAAAGCCAGCTCTTGCTGGTCAACCTGCTAACCTTTG  
301 -----+-----+-----+-----+-----+-----+ 360  
ACTCGGCGGACGACGCCGTGGCCTTTTCGGGTCGAGAACGACCAAGTTGGACGATTGGAAC

c S R L L R H R K A Q L L L V N L L T F G -

GCCTGGAGGTGTGTTTGGCCGAGGCATCACCTATGTGCCGCTCTGCTGCTGGAAGTGG  
361 -----+-----+-----+-----+-----+-----+ 420  
CGGACCTCCACAAACCGGCGTCCGTAGTGGATACACGGCGGAGACGACGACCTTCACC

c L E V C L A A G I T Y V P P L L L E V G -

GGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCT  
421 -----+-----+-----+-----+-----+-----+ 480  
CCCATCTCCTCTTCAAGTACTGGTACCACGACCCGTAACCAGGTACGACCCGGACACAGA

c V E E K F M T M V L G I G P V L G L V C -

GTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCGGC  
481 -----+-----+-----+-----+-----+-----+ 540  
CACAGGGCGAGGATCCGAGTCCGTACTGGTGACCGCACCTGCGATACCGGCGGCGGCCG

c V P L L G S A S D H W R G R Y G R R R P -

CCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGGCCG  
541 -----+-----+-----+-----+-----+-----+ 600  
GGAAGTAGACCCGTGACAGGAACCCGTAGGACGACTCGGAGAAAGAGTAGGGTTCCCGGC

c F I W A L S L G I L L S L F L I P R A G -

GCTGGCTAGCAGGGCTGCTGTGCCCGGATCCCAGGCCCTGGAGCTGGCACTGCTCATCC  
601 -----+-----+-----+-----+-----+-----+ 660  
CGACCGATCGTCCCGACGACACGGGCCCTAGGGTCCGGGGACCTCGACCGTGACGAGTAGG

c W L A G L L C P D P R P L E L A L L I L -

TGGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGC  
661 -----+-----+-----+-----+-----+-----+ 720  
ACCCGACCCCCGACGACCTGAAGACACCGGTCCACACGAAGTGAGGTGACCTCCGGGACG

c G V G L L D F C G Q V C F T P L E A L L -

# FIGURE 4 – continued

TCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCCTACTCTGTCTATGCCTTCA  
 721 -----+-----+-----+-----+-----+-----+-----+ 780  
 AGAGACTGGAGAAGGCCCTGGGCCTGGTGACAGCGGTCCGGATGAGACAGATACGGAAGT  
 C S D L F R D P D H C R Q A Y S V Y A F M -  
 TGATCAGTCTTGGGGGCTGCCTGGGCTACCTCCTGCCTGCCATTGACTGGGACACCAGTG  
 781 -----+-----+-----+-----+-----+-----+-----+ 840  
 ACTAGTCAGAACCCCGACGGACCCGATGGAGGACGGACGGTAACCTGACCCTGTGGTCAC  
 C I S L G G C L G Y L L P A I D W D T S A -  
 CCCTGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCCCTCATCT  
 841 -----+-----+-----+-----+-----+-----+-----+ 900  
 GGGACCGGGGGATGGACCCGTGGGTCTCTCACGGAGAAACCGGACGAGTGGGAGTAGA  
 C L A P Y L G T Q E E C L F G L L T L I F -  
 TCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGCAGCGTGGGCCCCACCG  
 901 -----+-----+-----+-----+-----+-----+-----+ 960  
 AGGAGTGGACGCATCGTCGGTGTGACGACCACCGACTCCTCCGTCGCGACCCGGGGTGGC  
 C L T C V A A T L L V A E E A A L G P T E -  
 AGCCAGCAGAAGGGCTGTCGGCCCCCTCCTTGTGCCCCACTGCTGTCCATGCCGGGCCC  
 961 -----+-----+-----+-----+-----+-----+-----+ 1020  
 TCGGTCGTCTTCCCACAGCCGGGGGAGGAACAGCGGGGTGACGACAGGTACGGCCCCGG  
 C P A E G L S A P S L S P H C C P C R A R -  
 GCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCCGCA  
 1021 -----+-----+-----+-----+-----+-----+-----+ 1080  
 CGAACCAGAAAGGCCTTGGACCCGCGGACGAAGGGGCCGACGTGGTCGACACGACGGCGT  
 C L A F R N L G A L L P R L H Q L C C R M -  
 TGCCCCGACCCCTGCGCCGGCTCTTCGTGGCTGAGCTGTGCAGCTGGATGGCACTCATGA  
 1081 -----+-----+-----+-----+-----+-----+-----+ 1140  
 ACGGGGCGTGGGACGCGGCCGAGAAGCACCGACTCGACACGTGACCTACCGTGAGTACT  
 C P R T L R R L F V A E L C S W M A L M T -  
 CCTTCACGCTGTTTTACACGGATTTCTGTTGGGCGAGGGGCTGTACCAGGGCGTGCCAGAG  
 1141 -----+-----+-----+-----+-----+-----+-----+ 1200  
 GGAAGTGCACAAAATGTGCCTAAAGCACCCGCTCCCCGACATGGTCCCGCACGGGTCTC  
 C F T L F Y T D F V G E G L Y Q G V P R A -  
 CTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCCGATGGGCAGCCTGG  
 1201 -----+-----+-----+-----+-----+-----+-----+ 1260  
 GACTCGGCCCGTGGCTCCGGGCCTCTGTGATACTACTCCGCAAGCCTACCCGTGCGACC  
 C E P G T E A R R H Y D E G V R M G S L G -  
 GGCTGTTCTGTCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCATGGACCGGCTGGTGC  
 1261 -----+-----+-----+-----+-----+-----+-----+ 1320  
 CCGACAAGGACGTACGCGGTAGAGGGACCAGAAGAGAGACCAGTACCTGGCCGACCACG  
 C L F L Q C A I S L V F S L V M D R L V Q -  
 AGCGATTCCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCG  
 1321 -----+-----+-----+-----+-----+-----+-----+ 1380  
 TCGCTAAGCCGTGAGCTCGTCAGATAAACCGGTACACCGTCGAAAGGGACACCGACGGC  
 C R F G T R A V Y L A S V A A F P V A A G -

FIGURE 4 - continued

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GTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACCGGGT
1381 -----+-----+-----+-----+-----+-----+ 1440
CACGGTGTACGGACAGGGTGTACACCCGCACCACTGTGAAGTCGGCGGGAGTGGCCCA
c      A T C L S H S V A V V T A S A A L T G F -
TCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCTCTACCACCGGGAGA
1441 -----+-----+-----+-----+-----+-----+ 1500
AGTGGAAAGAGTCGGGACGTCTAGGACGGGATGTGTGACCGGAGGAGATGGTGGCCCTCT
c      T F S A L Q I L P Y T L A S L Y H R E K -
AGCAGGTGTTCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGCC
1501 -----+-----+-----+-----+-----+-----+ 1560
TCGTCCACAAGGACGGGTTTATGGCTCCCTGTGACCTCCACGATCGTCACTCCTGTGCG
c      Q V F L P K Y R G D T G G A S S E D S L -
TGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGG
1561 -----+-----+-----+-----+-----+-----+ 1620
ACTACTGGTCGAAGGACGTTCCGGGATTTCGGACCTCGAGGGAAGGGATTACCTGTGCACC
c      M T S F L P G P K P G A P F P N G H V G -
GTGCTGGAGGCGAGTGGCCTGCTCCCACCTCCACCCGCGCTCTGCGGGGCTCTGCCTGTG
1621 -----+-----+-----+-----+-----+-----+ 1680
CACGACCTCCGTCACCGGACGAGGGTGGAGGTGGGCGCGAGACGCCCCGAGACGGACAC
c      A G G S G L L P P P P A L C G A S A C D -
ATGTCTCCGTACGTGTGGTGGTGGGTGAGCCACCGAGGCCAGGGTGGTTCCGGGGCCGGG
1681 -----+-----+-----+-----+-----+-----+ 1740
TACAGAGGCATGCACACCACCCACTCGGGTGGCTCCGGTCCCACCAAGGCCCGGCC
c      V S V R V V V G E P T E A R V V P G R G -
GCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCTGCTGTCCCAGGTGGCCCCAT
1741 -----+-----+-----+-----+-----+-----+ 1800
CGTAGACGGACCTGGAGCGGTAGGACCTATCACGGAAGGACGACAGGGTCCACCGGGGTA
c      I C L D L A I L D S A F L L S Q V A P S -
CCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTG
1801 -----+-----+-----+-----+-----+-----+ 1860
GGGACAAATACCCGAGGTAACAGGTTCGAGTCGGTCAGACAGTGACGGATATACCACAGAC
c      L F M G S I V Q L S Q S V T A Y M V S A -
CCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAGCG
1861 -----+-----+-----+-----+-----+-----+ 1920
GGCGTCCGGACCCAGACCAGCGGTAAATGAAACGATGTGTCCATCATAAACTGTTCTCGC
c      A G L G L V A I Y F A T Q V V F D K S D -
ACTTGGCCAAATACTCAGCGTAGAAAACCTTCCAGCACATTGGGGTGGAGGGCCTGCCTCA
1921 -----+-----+-----+-----+-----+-----+ 1980
TGAACCGGTTTATGAGTCGCATCTTTTGAAGGTTCGTGTAACCCACCTCCCGGACGGAGT
c      L A K Y S A * -
CTGGGTCCCAGCTCCCCGCTCCTGTTAGCCCCATGGGGCTGCCGGGCTGGCCGCCAGTTT
1981 -----+-----+-----+-----+-----+-----+ 2040
GACCCAGGGTCGAGGGGCGAGGACAATCGGGGTACCCCGACGGCCCGACCGGCGGTCAAA

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# FIGURE 4 - continued

2041 CTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCACCCTGTGCTGCTGAGGTGCGTAGC 2100  
 -----+-----+-----+-----+-----+-----+-----+  
 GACAACGACGGTTTCATTACACCGAGAGACGACGGTGGGACACGACGACTCCACGCATCG  
 TGCACAGCTGGGGGCTGGGGCGTCCCTCTCTCTCTCCCACTCTCTAGGGCTGCCTGAC  
 2101 -----+-----+-----+-----+-----+-----+-----+ 2160  
 ACGTGTGACCCCCGACCCCGAGGGAGAGGAGAGAGGGGTGAGAGATCCCGACGGACTG  
 TGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGCCAGAAGGGCTCCAT  
 2161 -----+-----+-----+-----+-----+-----+-----+ 2220  
 ACCTCCGAAGGTTCCCCCAAAGTCAGACCTGAATATGTCCCTCCGGTCTTCCCCGAGGTA  
 GCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGCCT  
 2221 -----+-----+-----+-----+-----+-----+-----+ 2280  
 CGTGACCTTACGCCCCCTGAGACGTCCACCTAATGGGTCCGAGTCCCAATTGTCGATCGGA  
 CCTAGTTGAGACACACCTAGAGAAGGGTTTGGGAGCTGAATAAACTCAGTCACCTGGT  
 2281 -----+-----+-----+-----+-----+-----+-----+ 2340  
 GGATCAACTCTGTGTGGATCTCTTCCCAAAACCCTCGACTTATTTGAGTCAGTGGACCA  
 TTCCCATCTCTAAGCCCCCTTAACCTGCAGCTTCGTTTAAATGTAGCTCTTGCATGGGAGTT  
 2341 -----+-----+-----+-----+-----+-----+-----+ 2400  
 AAGGGTAGAGATTGCGGAATTGGACGTGAAGCAAATTACATCGAGAACGTACCCTCAA  
 TCTAGGATGAAACACTCTCCATGGGATTGGAACATATGAAAGTTATTTGTAGGGGAAGA  
 2401 -----+-----+-----+-----+-----+-----+-----+ 2460  
 AGATCCTACTTTGTGAGGAGGTACCTAAACTTGTATACTTTCAATAAACATCCCCTTCT  
 GTCCTGAGGGGCAACACACAAGAACCAGGTCCCTCAGCCACAGCACTGTCTTTTGTCT  
 2461 -----+-----+-----+-----+-----+-----+-----+ 2520  
 CAGGACTCCCCGTTGTGTGTTCTTGGTCCAGGGGAGTCGGGTGTCGTGACAGAAAAACGA  
 GATCCACCCCCCTCTTACCTTTTATCAGGATGTGGCCTGTTGGTCTTCTGTTGCCATCA  
 2521 -----+-----+-----+-----+-----+-----+-----+ 2580  
 CTAGGTGGGGGGAGAATGGAATAATAGTCTACACCGACAACCAGGAAGACAACGGTAGT  
 CAGAGACACAGGCATTTAAATATTTAACTTATTTATTTAAACAAAGTAGAAGGGAATCCAT  
 2581 -----+-----+-----+-----+-----+-----+-----+ 2640  
 GTCTCTGTGTCCGTAATTTATAAATTGAATAAATAAATGTTTCATCTTCCCTTAGGTA  
 TGCTAGCTTTTCTGTGTTGGTGTCTAATATTTGGGTAGGTGGGGGATCCCCAACAAATCA  
 2641 -----+-----+-----+-----+-----+-----+-----+ 2700  
 ACGATCGAAAAGACACAACCACAGATTATAAACCCATCCACCCCCCTAGGGGTGTTAGT  
 GGTCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCTTCTCTCTGCGGT  
 2701 -----+-----+-----+-----+-----+-----+-----+ 2760  
 CCAGGGGACTCTATCGACCAGTAACCCGACTAGTAACGGTCTTAGAAGAAGAGGACCCCA  
 CTGGCCCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAAATGATAAT  
 2761 -----+-----+-----+-----+-----+-----+-----+ 2820  
 GACCGGGGGGTTTACGGATTGGGTCTGGAACCTTTAAGATGAGTAGGGTTTACTATTA  
 TCCAAATGCTGTTACCCAAGGTTAGGGTGTGAAGGAAGGTAGAGGTGGGGCTTCAGGT  
 2821 -----+-----+-----+-----+-----+-----+-----+ 2880  
 AGGTTTACGACAATGGGTTCGAATCCCACTTCTTCCATCTCCACCCCGAAGTCCA  
 CTCAACGGCTTCCCTAACCAACCCCTCTTCTCTTGGCCCAGCCTGGTTCCCCCACTTCCA  
 2881 -----+-----+-----+-----+-----+-----+-----+ 2940  
 GAGTTGCCGAAGGGATTGTTGGGGAGAAGAGAACCGGTGCGACCAAGGGGGGTGAAGGT  
 CTCCCCCTTACTCTCTCTAGGACTGGGCTGATGAAGGCACTGCCAAAATTTCCCTTACC  
 2941 -----+-----+-----+-----+-----+-----+-----+ 3000  
 GAGGGGAGATGAGAGAGATCTGACCCGACTACTTCCGTGACGGGTTTAAAGGGGATGG

# FIGURE 4 - continued

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3001 CCCAACTTTCCCCTACCCCCAACTTTCCCCACCAGCTCCACAACCCTGTTTGGAGCTACT
-----+-----+-----+-----+-----+-----+ 3060
GGGTTGAAAGGGGATGGGGGTTGAAAGGGGTGGTCGAGGTGTTGGGACAAACCTCGATGA

GCAGGACCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCCATCTCAGCCCCCAGAGT
3061 -----+-----+-----+-----+-----+-----+ 3120
CGTCCTGGTCTTCGTGTTTCACGCCAAAGGGTTCGGAAACAGGTAGAGTCGGGGGTCTCA

ATATCTGTGCTTGGGGAATCTCACACAGAACTCAGGAGCACCCCCTGCCTGAGCTAAGG
3121 -----+-----+-----+-----+-----+-----+ 3180
TATAGACACGAACCCCTTAGAGTGTGTCTTTGAGTCCTCGTGGGGACGGACTCGATTCC

GAGGTCTTATCTCTCAGGGGGGGGTTTAAGTGCCGTTTGCAATAATGTCGTCTTATTTAT
3181 -----+-----+-----+-----+-----+-----+ 3240
CTCCAGAATAGAGAGTCCCCCCCCAAATTCACGGCAAACGTTATTACAGCAGATAAATA

TTAGCGGGGTGAATATTTTATACTGTAAGTGAGCAATCAGAGTATAATGTTTATGGTGAC
3241 -----+-----+-----+-----+-----+-----+ 3300
AATCGCCCCACTTATAAAATATGACATTCACTCGTTAGTCTCATATTACAAATACCACTG

AAAATTAAAGGCTTTCTTAT
3301 -----+-----+ 3320
TTTTAATTCCGAAAGAATA

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**Figure 5**  
**Expression of Prost 3 in Human Tissue**

